

101573999

101573999 30 MAR 2006

SEQUENCE LISTING

<110> Bayer CropScience GmbH

<120> Plants with increased activity of a Class 3 branching enzyme

<130> BCS 03-5005-PCT

<150> EP 03090324.9

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

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Met Ser Thr Gly Tyr Glu Leu Met Gly Met His Arg Asn Ile Gln His			
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Gly His Phe Gly His Asp Asp Tyr Gly Tyr Trp Phe Ile Ile Leu Glu			
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Asp Lys Leu Arg Glu Gly Glu Pro Asp Lys Leu Tyr Phe Gln Gln			
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Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly Asp Thr Gly Ile Thr Val			
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Gly Ser Lys His Arg Val Tyr Phe Asn Thr Pro Asn Gly Pro Leu Glu			
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635		640		645
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Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
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Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp
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Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly
195 200 205

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325 330 335

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370 375 380

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Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
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Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly

690

695

700

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Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
740 745 750

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755 760 765

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770 775 780

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785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
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Gln Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg				
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Cys Ser Ala Thr Glu Gln Pro Pro Gln Arg Arg Lys Gln Arg Pro				
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180 185 190				

gat aaa ttg tat ttt caa cag tac aat tat gcg gag gac tat ggt aaa Asp Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys 195 200 205	625
ggt gac acg ggt att acc gtc gag gaa atc ttt aaa aaa gca aat gat Gly Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp 210 215 220	673
gag tat tgg gaa cct gga gaa gat cgc ttc att aaa tca cgt tat gag Glu Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu 225 230 235	721
gtg gca gca aag tta tat gag gaa atg ttc gga cca aat gga cct caa Val Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln 240 245 250 255	769
aca gaa gag gaa cta gaa gca atg cct gat gca gct aca cga tac aaa Thr Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys 260 265 270	817
act tgg aaa gag caa caa aaa gag gat ccg gca agc aat ttg cca tcg Thr Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser 275 280 285	865
tat gat gtg gta gat agt gga aaa gaa tat gat att tac aat att ata Tyr Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile 290 295 300	913
ggt gat cct gaa tcg ttt aag aaa ttt cgt atg aaa cag cct cct att Gly Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile 305 310 315	961
gct tac tgg tta gaa act aaa aag gga agg aaa ggc tgg tta cag aaa Ala Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys 320 325 330 335	1009
tat atg cct gct tta cat gga agc aaa tac agg gtg tat ttt aac Tyr Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn 340 345 350	1057
aca cca aat ggg cct ctt gaa cga gtt cct gcg tgg gcc aat ttt gtc Thr Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val 355 360 365	1105
att cca gat gca ggc ggg atg gca tta gca gtc cat tgg gaa cca cct Ile Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro 370 375 380	1153
cct gaa tat gct tat aaa tgg aaa cac aag cta cca gtc aag cct aag Pro Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys 385 390 395	1201
tcc ttg cgc ata tat gaa tgt cat gtt ggc atc tct ggc cag gaa cca Ser Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro 400 405 410 415	1249

aaa gtt tca tct ttc aat gat ttt att agc aag gtc ctt ccg cat gta Lys Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val 420 425 430	1297
aaa gaa gct gga tac aat gca ata caa att att gga gtt gtt gag cac Lys Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His 435 440 445	1345
aag gat tat ttc act gtt gga tat aga gtg acc aat ttt tat gct gtt Lys Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val 450 455 460	1393
agt agc cgt tat ggc aca ccg gat gac ttc aag cgc ttg gtt gat gaa Ser Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu 465 470 475	1441
gca cat ggg ctt gga ctg ctt gtc ttt ttg gag att gtg cac tct tat Ala His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr 480 485 490 495	1489
gca gca gca gat gaa atg gtt ggg tta tct ctt ttt gat gga gca aat Ala Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn 500 505 510	1537
gat tgc tat ttc cac act ggt aaa cgt gga cac cac aaa ttc tgg ggc Asp Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly 515 520 525	1585
aca cggttccaaaatggagatcttcatgttctgtcacttttctt Thr Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu 530 535 540	1633
tca aat ctg aac tgg tgg gtg gag gag tat cat gtc gat ggc ttc cat Ser Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His 545 550 555	1681
ttt cat tcg ctc tcg tcc atg ttg tat acg cat aat gga ttt gct tca Phe His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser 560 565 570 575	1729
ttt act ggt gac atg gat gaa tac tgt aac caa tat gtt gac aag gag Phe Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu 580 585 590	1777
gcc tta ttg tac ctc ata tta gca aat gaa gta tta cat gct ctt cat Ala Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His 595 600 605	1825
cct aat gtg atc acg att gct gag gat gca act ctg tat cct gga ctc Pro Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu 610 615 620	1873
tgc gat cca aca tct caa ggt gga ctg ggc ttt gat tat ttt gcc aat Cys Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn 625 630 635	1921
ctt tct gcc tca gag atg tgg ctt gca tta ctt gaa aat act cct gat	1969

Leu Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp				
640	645	650	655	
cat gaa tgg tgc atg agt aag att gtt agc aca tta gtg ggc gat aga				2017
His Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg				
660	665	670		
caa aat act gat aaa atg ctt ttg tat gca gaa aat cac aac cag tcc				2065
Gln Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser				
675	680	685		
att tct gga ggt cgt tcc ttc gca gaa ata ctg att ggt aac tcc ttg				2113
Ile Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu				
690	695	700		
ggg aaa tcc tcc ata tca caa gag tca tta ctt aga ggc tgc tcg tta				2161
Gly Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu				
705	710	715		
cac aag atg atc aga tta att aca tct aca att ggt ggt cat gca tac				2209
His Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr				
720	725	730	735	
ctc aac ttc atg ggc aat gaa ttt ggt cac cca aag aga gta gag ttt				2257
Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe				
740	745	750		
cca atg tca agc aac aat ttc tcc ttt tca ctg gct aac cgt cgc tgg				2305
Pro Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp				
755	760	765		
gat cta ttg gaa gat gtt gta cat tat caa ttg ttc tca ttt gat aag				2353
Asp Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys				
770	775	780		
ggg atg atg gac ttg gat aaa aat ggg aga att ttg tcc aga ggt ctt				2401
Gly Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu				
785	790	795		
gcc aac att cac cat gtc aat gat act acc atg gtg att tct tac ttg				2449
Ala Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu				
800	805	810	815	
aga ggt ccc aat ctc ttt gtg ttc aac ttt cat cct gtc aat tca tat				2497
Arg Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr				
820	825	830		
gaa aga tac att ata ggt gtg gaa gaa gct gga gag tat caa gtc aca				2545
Glu Arg Tyr Ile Ile Gly Val Glu Ala Gly Glu Tyr Gln Val Thr				
835	840	845		
tta aat aca gat gaa aac aag tat ggt ggt aga gga cta ctt ggc cat				2593
Leu Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His				
850	855	860		
gat cag aat att caa aga acc att agt aga aga gct gat gga atg aga				2641
Asp Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg				

865	870	875	
ttt tgc ttg gaa gtg cct ctg cca agt aga agt gct cag gtc tac aag Phe Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys 880	885	890	2689
ttg acc cga att cta aga gca tgatcactct agtaatcaaa gtgcctcata Leu Thr Arg Ile Leu Arg Ala 900			2740
tgatgacaca aaaggaaagg ttctacattg cccttacact gatcaatatt gacaccttc cgaggtgagt ttctgtgatt cttgagcaga ctgtggcta gtcaattatc atgaactttt gccttcagca tccggatagt cgcttctcct gtgcaatgag ggcatggacg aattttttt tggcttgtca tgggggtcat aagcatccgc cagattaaga tttcacaggg ctcgagtaaa accatcaactt actttaagga tacacaaaca caccaacggg gtgcaggctc tgataacctc taaagtg			2800
			2860
			2920
			2980
			3040
			3047
<210> 6			
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<400> 6			
Met Leu Ser Leu Ser Asp Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp 1 5 10 15			
Ser Arg Leu Ser Phe Leu Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln 20 25 30			
Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys 35 40 45			
Ser Ala Thr Glu Gln Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu 50 55 60			
Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly Phe 65 70 75 80			
Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg 85 90 95			
Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg 100 105 110			

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
145 150 155 160

Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
165 170 175

Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Pro Asp
180 185 190

Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys Gly
195 200 205

Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu
210 215 220

Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val
225 230 235 240

Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
260 265 270

Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser Tyr
275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
290 295 300

Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
325 330 335

Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr
340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
355 360 365

Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
420 425 430

Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys
435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
515 520 525

Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser
530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe

	565	570	575
Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala			
580	585		590
Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro			
595	600		605
Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu Cys			
610	615		620
Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu			
625	630	635	640
Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His			
645	650		655
Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln			
660	665		670
Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile			
675	680		685
Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly			
690	695		700
Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His			
705	710	715	720
Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu			
725	730		735
Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro			
740	745		750
Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp			
755	760		765
Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Gly			
770	775		780
Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala			
785	790	795	800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
835 840 845

Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
850 855 860

Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
865 870 875 880

Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
885 890 895

Thr Arg Ile Leu Arg Ala
900